

RESULT 1

AAB13956

ID AAB13956 standard; protein; 1402 AA.

XX

AC

AAB13956;

XX

DT

15-JUN-2007 (revised)

DT

16-NOV-2000 (first entry)

XX

DE

Neurospora crassa QDE-1 protein.

XX

KW

Gene silencing; quelling deficient; qde-1; al-1; BOND_PC;

KW

RNA-dependent RNA polymerase;

KW

RNA-dependent RNA polymerase [Neurospora crassa]; G03968.

XX

OC

Neurospora crassa.

XX

PN

WO200050581-A2.

XX

PD

31-AUG-2000.

XX

PF

16-FEB-2000; 2000WO-IT000048.

XX

PR

22-FEB-1999; 99IT-RM000117.

XX

PA

(UVRO-) UNIV ROMA LA SAPIENZA.

XX

PI

Macino G, Cogoni C;

XX

DR

WPI; 2000-579171/54.

DR

N-PSDB; AAA65171.

DR

PCINCB; g14803727.

XX

PT

Novel polynucleotide encoding a polypeptide which has a silencing

PT

activity and comprising a RNA-dependent RNA polymerase domain.

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PS

Claim 21; Fig 4; 48pp; English.

XX

CC

The present sequence is the Neurospora crassa QDE-1 protein. This protein

CC

has gene silencing activity. The qde-1 gene was isolated by mutational

CC

analysis of an al-1 transgenic strain. This strain had an albino

CC

phenotype resulting from post-transcriptional silencing of the endogenous

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al-1 gene. Reversion of this phenotype indicated a mutation in a

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silencing gene. The silencing gene, qde-1, could then be isolated.

CC

Modulation of qde-1 expression may be used to inactivate genes and to

CC

silence suppression of genes

CC

CC

Revised record issued on 15-JUN-2007 : Enhanced with precomputed

CC

information from BOND.

XX

SQ

Sequence 1402 AA;

Query Match 100.0%; Score 7397; DB 3; Length 1402;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MNPITPRKRNSPVVEEINRLNNDYNLGLQCVDTTLTTPHRRKELAESDEDFGRHDKIYRA	60
Db	1	MNPITPRKRNSPVVEEINRLNNDYNLGLQCVDTTLTTPHRRKELAESDEDFGRHDKIYRA	60
Qy	61	LNFLYWRKDDSLNQAEANFFIEAKAASSNWVPAHADPDTLPWSKEPPRAATAGQWALQ	120
Db	61	LNFLYWRKDDSLNQAEANFFIEAKAASSNWVPAHADPDTLPWSKEPPRAATAGQWALQ	120
Qy	121	TVLLEVLNRFMPNNPTPGRTFGRTLSPGSLSRPTSTNTRKDEPANVTADPPKRSLT	180
Db	121	TVLLEVLNRFMPNNPTPGRTFGRTLSPGSLSRPTSTNTRKDEPANVTADPPKRSLT	180
Qy	181	RSATGPPHGAALPLKFPDPVNTGSKRPSLESENLNQCTKRAKGLSDNVAAAAAPPVPI	240
Db	181	RSATGPPHGAALPLKFPDPVNTGSKRPSLESENLNQCTKRAKGLSDNVAAAAAPPVPI	240

Qy	241	ASALDKVPIRRHANTRDPTATGHRRAQVDSFDTSGTSGYSSVFSACRHNQSTTQSSFE	300
Db	241	ASALDKVPIRRHANTRDPTATGHRRAQVDSFDTSGTSGYSSVFSACRHNQSTTQSSFE	300
Qy	301	APPSQPREKRPVDATVFEAGHLIESPSKGRITKSHIDNQPLSSSSQGTSTFTYTESPPS	360
Db	301	APPSQPREKRPVDATVFEAGHLIESPSKGRITKSHIDNQPLSSSSQGTSTFTYTESPPS	360
Qy	361	SGGEGAIPEPSRSNGLARSEECARSQVQHAPVVAARLRNIWPKFKPWLHEAPLAVAMEV	420
Db	361	SGGEGAIPEPSRSNGLARSEECARSQVQHAPVVAARLRNIWPKFKPWLHEAPLAVAMEV	420
Qy	421	TRLFMHCKVLEDESLGLKYDPSMSTARDVTDIMKTLYRLDAFRGKPFPEKFPNDVFVTA	480
Db	421	TRLFMHCKVLEDESLGLKYDPSMSTARDVTDIMKTLYRLDAFRGKPFPEKFPNDVFVTA	480
Qy	481	MTGNFESKGSAGVLSAVLDYNPDNSPTIAPLYLVKLPLMFEGQCRLTRRFGRPFPEILI	540
Db	481	MTGNFESKGSAGVLSAVLDYNPDNSPTIAPLYLVKLPLMFEGQCRLTRRFGRPFPEILI	540
Qy	541	PSPSTSPSPVFPVSKQPGAVEEIQWLTMGQHSLVGRQWRAFFAKDAGYRKPLREFQLR	600
Db	541	PSPSTSPSPVFPVSKQPGAVEEIQWLTMGQHSLVGRQWRAFFAKDAGYRKPLREFQLR	600
Qy	601	AEDPKPIIKERVHFFAETGITFRPDVFKTRSVVPAEEVEQRTFKVQMLDWLLQLDNN	660
Db	601	AEDPKPIIKERVHFFAETGITFRPDVFKTRSVVPAEEVEQRTFKVQMLDWLLQLDNN	660
Qy	661	TWQPHLKLFSRIQLGLSKTYAIMTLEPHQIRHHKTDLLSPSGTEVMNDGVRMSRSVAK	720
Db	661	TWQPHLKLFSRIQLGLSKTYAIMTLEPHQIRHHKTDLLSPSGTEVMNDGVRMSRSVAK	720
Qy	721	RIRDVLGLGVPSAVQGRFGSAGKGMWIDVDDTGDGDMETYPQKRWECDFVDKHQRTL	780
Db	721	RIRDVLGLGVPSAVQGRFGSAGKGMWIDVDDTGDGDMETYPQKRWECDFVDKHQRTL	780
Qy	781	EVRSVASELSAGLNLQLLVLEDRAROKVQRQAIGORLINDLQRFSEQKHALNRPVE	840
Db	781	EVRSVASELSAGLNLQLLVLEDRAROKVQRQAIGORLINDLQRFSEQKHALNRPVE	840
Qy	841	FRQMWYESYSSRATRVSHGRVPFLAGLPDSQETLNFLMNSGFDPKKQKYLQDIAMDLOK	900
Db	841	FRQMWYESYSSRATRVSHGRVPFLAGLPDSQETLNFLMNSGFDPKKQKYLQDIAMDLOK	900
Qy	901	RKCDTLKSKLNIRVRSAYIYMIADFWGVLEENEVHVGFSSKFRDEEESFTLLSDCDVLV	960
Db	901	RKCDTLKSKLNIRVRSAYIYMIADFWGVLEENEVHVGFSSKFRDEEESFTLLSDCDVLV	960
Qy	961	ARSAHFPSDIQRVRAVFKPELHSLKDVIIIFSTKGQVPLAKKLGGDVGDMAMVWCDPE	1020
Db	961	ARSAHFPSDIQRVRAVFKPELHSLKDVIIIFSTKGQVPLAKKLGGDVGDMAMVWCDPE	1020
Qy	1021	IVDGFVNAEMPLEPDLISRYLKKDKTTFKQLMASHTGSAAKEQTTVDIMIQSFHFALQPN	1080
Db	1021	IVDGFVNAEMPLEPDLISRYLKKDKTTFKQLMASHTGSAAKEQTTVDIMIQSFHFALQPN	1080
Qy	1081	FLGMCTNYKERLCYINNVSNGKPAIILSSLVGNLVDSQKQIGVFNEASWQALRELLGGA	1140
Db	1081	FLGMCTNYKERLCYINNVSNGKPAIILSSLVGNLVDSQKQIGVFNEASWQALRELLGGA	1140
Qy	1141	LSLPDMYKSDSWLGRGEPHTIIDYLKFSIARPAIDKELEAFHNAMKAAKDDTGAHFWO	1200
Db	1141	LSLPDMYKSDSWLGRGEPHTIIDYLKFSIARPAIDKELEAFHNAMKAAKDDTGAHFWO	1200
Qy	1201	PDLASYITFFKEISDKSRSSALLFTLLKNRIGEVKEYGRLVKNKEMRSDKDPYFVRVWQ	1260
Db	1201	PDLASYITFFKEISDKSRSSALLFTLLKNRIGEVKEYGRLVKNKEMRSDKDPYFVRVWQ	1260
Qy	1261	VVEHWCAITPEAMDKSGANYDQKVRILLESFLADREMNTHWALLRASAFKLYYHKSPPK	1320

Db	1261	VYEKWCATTPEAMDKSGANYDSKVIRLLELSFLADREMNTWALLRASTAFKLYYHKSPKF	1320
Qy	1321	VWQMAGRQLAYIKAQMTSRPGE GAPALMTAFMYAGLMPDKKFTKQYVARLEGDGSEYPDP	1380
Db	1321	VWQMAGRQLAYIKAQMTSRPGE GAPALMTAFMYAGLMPDKKFTKQYVARLEGDGSEYPDP	1380
Qy	1381	EVYEVLGDDDFDGIGFTGNGDY	1402
Db	1381	EVYEVLGDDDFDGIGFTGNGDY	1402